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ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTICTGATACCGAAACCACCGGTATGAACCAGATTGGT 75  
-----mutD-----  
M T A M S T A I T R Q I V L D T E T T G M N Q I G  
GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTCCGTTGAAGTGGTGAACCGTCGCCCTGACGGGCAATAAC 150  
-----mutD-----  
A H Y E G H K I I E I G A V E V N R R L T G N N  
TTCCATGTTTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTGGCGTACATGGTATTGCCGATGAATTT 225  
-----mutD-----  
F H V Y L K P D R L V D P E A F G V H G I A D E F  
TTGCTCGATAAGCCACGTTTGCCGAAGTAGCCGATGAGTTCAATGGACTATATTCCGCGCGGAGTTGGTGATC 300  
-----mutD-----  
L L D K P T F A E V A D E F M D Y I R G A E L V I  
CATAACGCGGTTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGATATTCGGAAGACCAAT 375  
-----mutD-----  
H N A A F D I G F M D Y E F S L L K R D I P K T N

FIG.-1A

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ACTTTCGTAAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAATGTTTCCCGTAAGCGCAACAGCCTCGATGCG 450

mutD

T F C K V T D S L A V A R K M F P G K R N S L D A

TTATGTGCTCGCTACGAAATAGATAACAGTAAACGACGCTGCACGGGGCATTACTCGATGCCCAGATCCTTGCG 525

mutD

L C A R Y E I D N S K R T L H G A L L D A O I L A

GAAGTTTATCTGGCGATGACCGGTGGTCAACGCTCGATGGCTTTTGGCATGGAAGGAGAGACACACAGCAACAA 600

mutD

E V Y L A M T G G O T S M A F A M E G E T O O O O

GGTGAAGCAACAATTCAGCGCATTGTACGTCAGGCAAGTAAGTTACGCGTTGTTTTGCGACAGATGAAGAGATT 675

mutD

G E A T I O R I V R Q A S K L R V V F A T D E E I

GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGCGGAAGTTGCCTCTGGCGAGCATAA 741

mutD

A A H E A R L D L V Q K K G G S C L W R A .

FIG. 1B

**FIG.-2A**

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310	GGCGGCAGCCCGCA	320	CGGACTGCCGGTAAAGGCA	330	TTGGTATTGCGGCCACCCAC	340	CCCGGGTGAT	Eb_429T.dna
310	GGCGGCAGCCCGCTCGACTCGGCTAAGGCA	320	TTGGTATTGCGGCCACCCAC	330	CCCGGGTGAT	340		Eb_GEBT.dna
370	CTGTACAGCTATGCCCGGTATCGAAACA	380	CACTCA	390	CCCGCTGCCCGCCCATTTAT	400	TGCGGTC	Eb_429T.dna
370	CTGTACAGCTATGCCCGGTATCGAAACA	380	CACTCA	390	CCCGCTGCCCGCCCATTTAT	400	TGCGGTC	Eb_GEBT.dna
430	AACACCA	440	CCCGGACCGCCAGCGAAGTCA	450	CCCGCCACTGCGTGCTGACTAACACCAAA	460		Eb_429T.dna
430	AACACCA	440	CCCGGACCGCCAGCGAAGTCA	450	CCCGCCACTGCGTGCTGACTAACACCAAA	460		Eb_GEBT.dna
490	ACCAAAGTAA	500	TTTGTGATTGTCA	510	GCTGGCGCAACCTGCCCTTCCGTTCCCATTAACGAT	520		Eb_429T.dna
490	ACCAAAGTAA	500	TTTGTGATTGTCA	510	GCTGGCGCAACCTGCCCTTCCGTTCCCATTAACGAT	520		Eb_GEBT.dna
550	CCGCTGCTGATCGGGCAAGCCCGCGGCTGACCGCCGCCACCCGGTATGGATGCCCTG	560		570		580		Eb_429T.dna
550	CCGCTGCTGATCGGGCAAGCCCGCGGCTGACCGCCGCCACCCGGTATGGATGCCCTG	560		570		580		Eb_GEBT.dna

FIG.-2B

**FIG.-2C**

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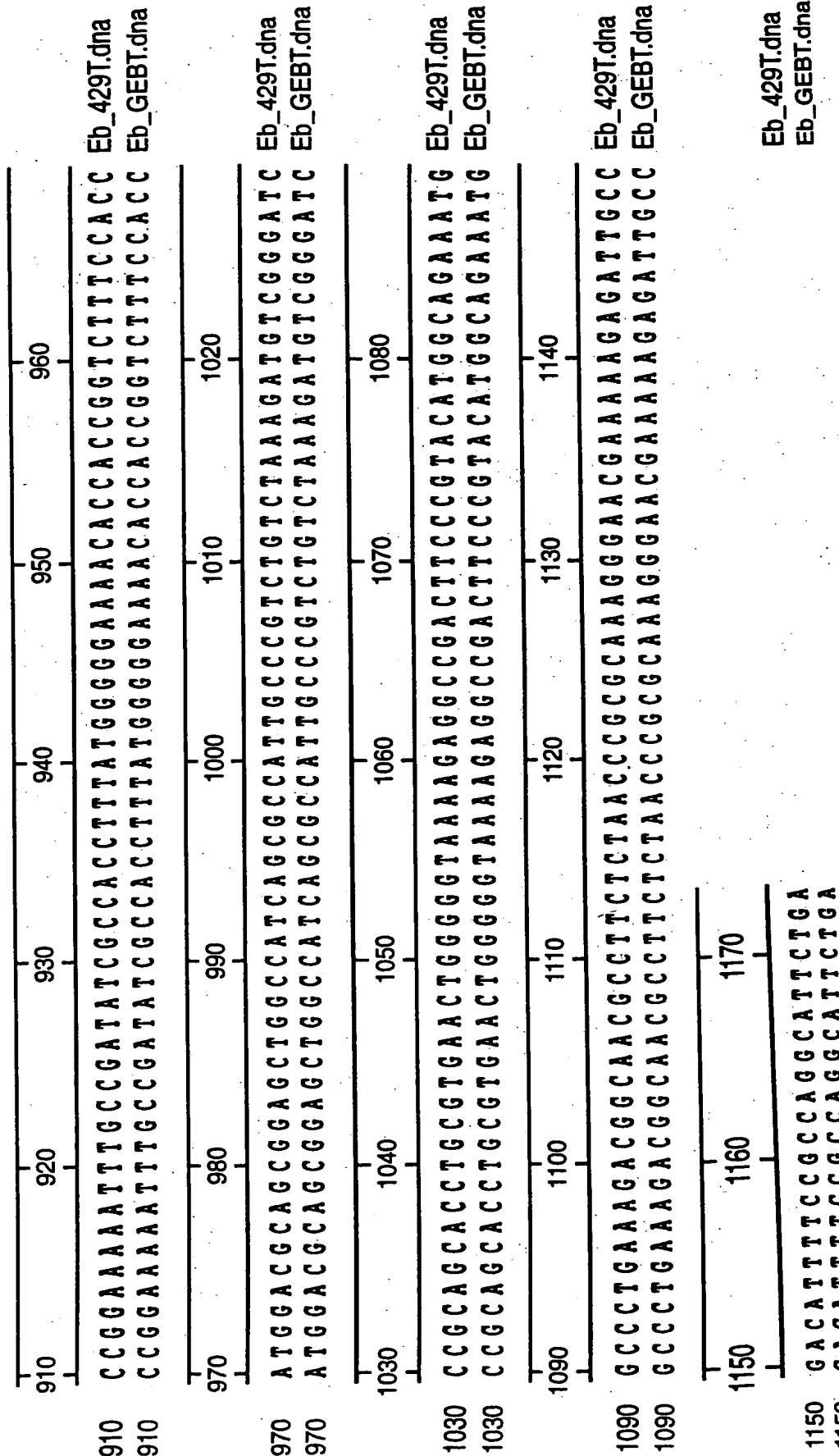


FIG.-2D

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	10	40	70	100	
10	MSYRMFDYLVPNVNFPGPGAVSVVGQRCQLLGKKALLVT Eb_429T.dna				
10	MSYRMFDYLVPNVNFPGPGAVSVVGQRCQLLGKKALLVT Eb_GEBT.dna				
	130	160	190	220	
130	DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVBPDPKDTN Eb_429T.dna				
130	DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGVBPDPKDTN Eb_GEBT.dna				
	250	280	310	340	
250	VLDGLAMFRKEQCDMIIITVGGGSPHDCGKGIGIGIAATHPGD Eb_429T.dna				
250	VLDGLAMFRKEQCDMIIITVGGGSPDCCGKGIGIGIAATHPGD Eb_GEBT.dna				
	370	400	430	460	
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK Eb_429T.dna				
370	LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK Eb_GEBT.dna				
	490	520	550	580	
490	TKVKFVI VSWRNLPVSINDP LLMIGKPA GLTAA TGMDAL Eb_429T.dna				
490	TKVKFVI VSWRNLPVSINDP LLMIGKPA GLTAA TGMDAL Eb_GEBT.dna				

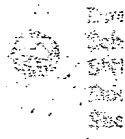
FIG.\_3A

610	THAVEAYISKDANPVT	640	670	700	Eb_429T.dna
610	THAVEAYISKDANPVT	640	670	700	Eb_GEBT.dna
730	LKARENMACASLLAGMAFN	760	790	820	Eb_429T.dna
730	LKARENMACASLLAGMAFN	760	790	820	Eb_GEBT.dna
850	HGVANAVLLPHVCRYNLI	880	910	940	Eb_429T.dna
850	HGVANAVLLPHVCRYNLI	880	910	940	Eb_GEBT.dna
970	MDAABELAISAIARLSK	1000	1030	1060	Eb_429T.dna
970	MDAABELAISAIARLSK	1000	1030	1060	Eb_GEBT.dna
1090	ALKDGNAPSNPRKGNBKE	1120	1150		Eb_429T.dna
1090	ALKDGNAPSNPRKGNBKE	1120	1150		Eb_GEBT.dna

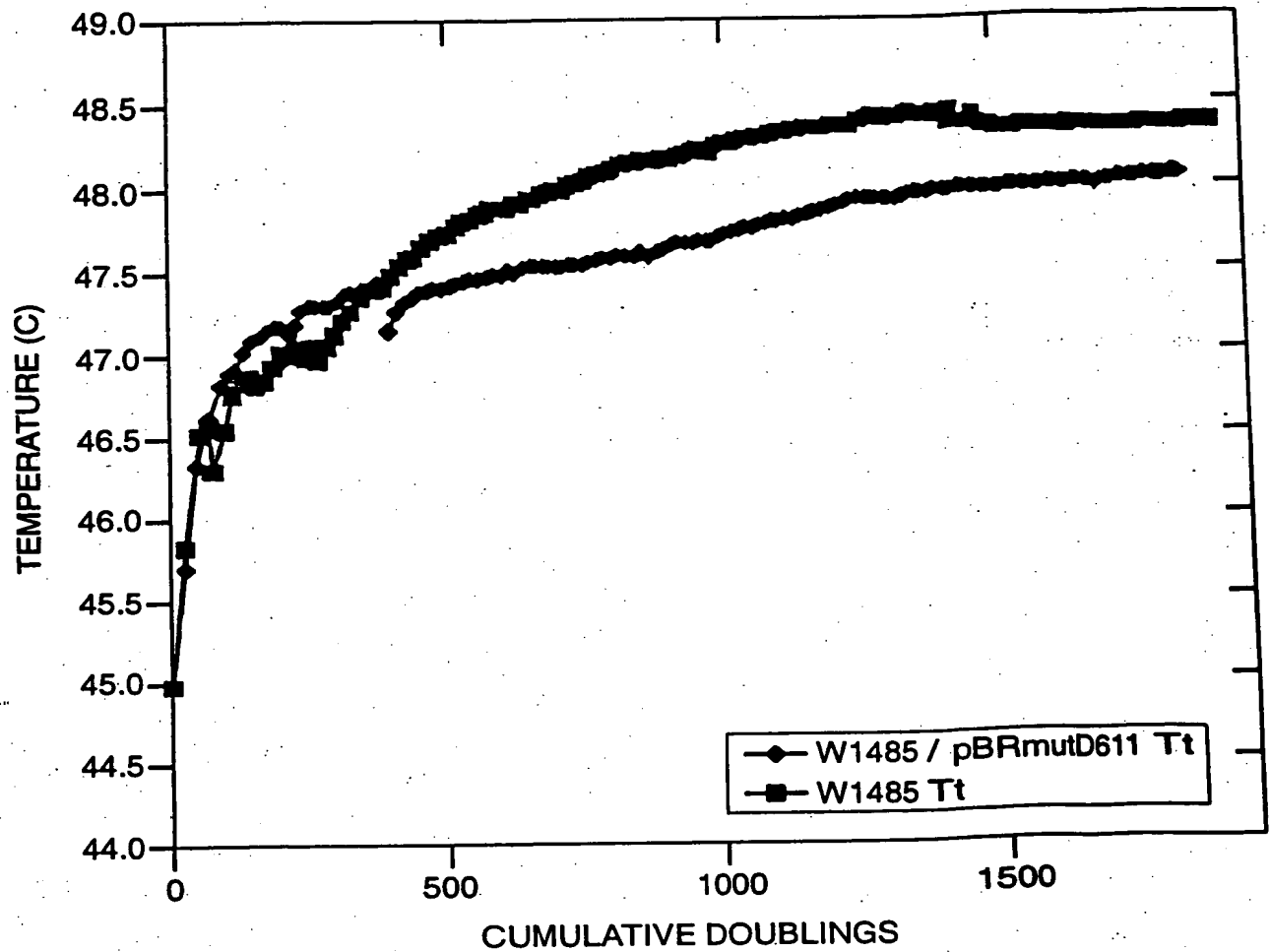
**Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.**

**FIG. 3B**





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**FIG. 4**

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